OM protein - protein search, using sw model

GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    December 13, 2002, 22:53:08; Search time 44 Seconds (without alignments)
117.983 Million cell updates/sec
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mixed-lineage prot
mixed-lineage prot
protein kinase ATN
protein kinase (EC
                                       S-receptor kinase
hypothetical prote
protein kinase hom
Receptor-like seri
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probable mitogen-a
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probable serine/th protein F12M16.4 [
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                                                                                               mixed-lineage protein kinase (EC 2.7.1.-) 3 - human Mixed-lineage protein kinase (EC 2.7.1.-) 3 - human MyAlternate names: protein kinase PTK1; protein kinase SPRK C; Species: Homo sapiens (man) C; Pate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C; Paccession: A53800; I58395 R; Callo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J. J. Biol. Chem. 269, 15092-15100, 1994 Mang, Z.; Gu, Q.; Godowski, P.J. A; Title: Identification and Characterization of SPRK, a novel src-homology 3 domain-c A; Reference number: A53800; MUID:94253068; PMID:8195146 A; Accession: A53800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: GDB:MLK1
A,Gross-references: GDB:141921; OMIN:600136
A,MCross-references: GDB:141921; OMIN:600136
A,MDP postition: 14924.3-14931
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protei C;Keywords: ATP; leucine zipper motif F;1-269/Domain: protein kinase homology <KIN>
F;1-269/Domain: catalytic <CAT>
F;9-17/Region: protein kinase ATP-binding motif F;289-310/Region: leucine zipper motif F;324-345/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mixed-lineage protein kinase 1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: $32467; JUD229
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur. J. Biochem. 213, 701-710, 1993
A;Title: Identification of a new family of human epithelial protein kinases containin
A;Reference number: $32467; MUID:93238756; PMID:84777742
A;Accession: $32467; MUID:93238756; PMID:84777742
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A; Residues: 1-394 <DO2>
A;Cross-references: GB:U07747; NID:g464027; PIDN:AAA19647.1; PID:g464028
R;Ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassam, N.J.
                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-847 <GAL>
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Pred. No. 1.2e-16;
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

283224

283224 seqs, 96134422 residues

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Perfect score:

US-09-659-737A-2 293

1 HRDIKAGNILLLEKIEHDDI.....

Database

PIR_73:*

pir1:*

Result

NO.

Score

Query Match

Length

DВ

SUMMARIES

239 231 216 127

111 111 108.5 107.5 107.5 107.5 107.5

106 105.5 105.5 105.5 104.5 104.5

H96731

114.5 111

124.5 124.5 124.5 121.5

JC2363 A55318 JC5399

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A:Map position: 19q13.1-19q13.2
C:Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 homology
C:Keywords: ATP. leucine zipper; phosphotransferase; serine/threonine-specific protein: 23-76/Domain: SH3 homology <SH3>
F:96-364/Domain: protein kinase homology <KIN>
F:104-112/Region: protein kinase ATP-pinding motif
F:384-405/Region: leucine zipper motif
F:449-440/Region: leucine zipper motif
F:449-463/Region: leucine zipper motif
F:449-463/Region: basic
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A.Molecule type: mrNA
A.Molecule type: mrNA
A.Residues: 1-461,'A','V',465-470,'S',472-806,'R',808-817,'A',819-954 <RES>
A.Residues: 1-461,'A','V',465-470,'S',472-806,'R',808-817,'A',819-954 <RES>
A.Gross-references: EMBL:248615; NID:9758592; PIDN:CAA88531.1; PID:9758593
R.Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
R.Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur. J. Biochem. 213, 701-710, 1993
Eur. J. Biochem. 213, 701-710, 1993
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C;Genetics:
A;Genetics:
A;Ge
F;125,145,222,224/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:362654; GDB:624810; OMIM:600137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Identification of a new family of human epithelial protein kinases containing A;Reference number: S32467; MUID:93238756; PMID:8477742 A;Accession: S32468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X90846; NID:g971419; PIDN:CAA62351.1; PID:g971420 R;Katch, M.; Hirai, M.; Sugimura, T.; Terada, M. Oncogene 10, 1447-1451, 195 A;FitLe: Cloning and characterization of MST, a novel (putative) serine/threonine kinase A;Reference number: 138044; MUID:95249256; PMID:7731697 A;Accession: 138044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mixed-lineage protein kinase 2 (BC 2.7.1.-) - human G;Species: Homo sapiens (man) C;Pate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999 C;Pate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999 C;Pate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999 C;Pate: 28-Oct-1995 #sequence_revision: S68178; 138044; S32468 R;DDTOW, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simps R;DDTOW, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.K.; Sutherland, G.R.; Simps Eur. J. Biochem. 234, 492-500, 1995
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A;Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 doma.
A;Reference number: 158395; MUID:94239754; PMID:8183572
A;Recession: 158395
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 244-464,'AQAAGRRQPHQPALWL' <DO2>
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A; Residues: 1-954 < DOR>
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A;Accession: S68178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-847 < RES>
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Similarity 77.8%;
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Pred. No. 1.6e-15;
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology cristal content kinase homology cristal content kinase homology cristal c
                                                                                                                                                           F;152/Active site: Lys #status predicted
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A; Residues: 1-668 < RED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: ZPK
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A; Introns: 170/1;
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A; Residues: 1-356 <BEV>
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A; Accession: T48206
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                                                 Query Match
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Best Local
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39; Conservative
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72.2%;
                                                 42.5%;
                                                 Score 124.5;
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                                          DB 2;
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A;Cross-references: EMBL:007358
A;Experimental source: brain
A;Note: the nucleotide sequence for this amino acid sequence is inconsistent with tha he codon ACC for residue 661 as Pro, the codon GAACCACCTCCTCA for residues 664-668 a C;Comment: This protein belongs to the family of non-receptor kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Feb-2001
C;Accession: JC3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 202, 613-620, 1994
A;Title: Cloning of a novel putative protein kinase having a leucine zipper domain fr
A;Reference number: JC2363; MUID:94311945; PMID:8037767
A;Accession: JC2363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase ATN1-like protein - Arabidopsis thaliana N;Alternate names: protein 720115.120 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 *sequence_revision 20-Apr-2000 *tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: cultivar Columbia; BAC clone T20L15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 HRDLKSINILILEAIENHNLADTVLKITDFGLAREWHKTTKMSAAGTYAWMAPE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               match 43.3%; Score 127; DB 2; Local Similarity 51.8%; Pred. No. 1.6e-05; es 29; Conservative 7. Processing the conservative for the conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRTTKMSTA--GTYAWMAPE 54
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the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 216; DB 1; Length 954; Pred. No. 5.7e-14;
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C; Comment:
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:U14636; NID:g602677; PIDN:AAA57280.1; PID:g602678
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold C;Keywords: ATP; leucine zipper; phosphotransferase
F;156-404/Domain: protein kinase homology <KIN>
F;156-404/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: ATP; phosphotransferase F;54-75,89-98/Region: glycine-rich F;156-454/Domain: kinase catalytic #status predicted <CAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: JC5399
R; Matsui, N.; Sarka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dual leucine zipper kinase (EC 2.7.-.-) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;156-404/Domain: protein kinase Homology when F;164-172/Region: protein kinase ATP-binding motif
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A; Residues: 1-888 < HOL>
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                                                                                                                                                                                                                                                                                   F;164-172/Region: protein kinase ATP-binding motif F;421-449/Region: leucine zipper motif F;472-500/Region: leucine zipper motif F;472-500/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Matsul, N.; Sarkar, G.; Shuto, T.; Marrs, J.; Bronk, J.T.; Mizuno, K.; Bolander, M.E. Blochem. Blophys. Res. Commun. 229, 571-576, 1996
A;Title: Identification of a dual leucine zipper kinase involved in rat fracture repair. A;Reference number: JC5399; MUID:97127443; PMID:8954939
A;Accession: JC5399
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A; Residues: 1-888 <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                                            ;557-888/Region: glycine-serine-proline rich #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment: This enzyme is involved in regulating cell function in the musculosketal syst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 HRDLKSPNML----ITYDDV----VKISDFGTSKELSDKSTKMSFAGTVAWMAPE 313
                             267 HRDLKSPNML----ITYDDV----VKISDFGTSKELSDKSTKMSFAGTVAWMAPE 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE 54
                                                                                  1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE 54
                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.5%; Score 124.5; DB 2; 50.9%; Pred. No. 6.9e-05;
                                                                                                                                                                            42.5%;
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                                                                                                                                        Score 124.5; DB 2;
Pred. No. 6.9e-05;
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                                                                                                                                                                                                   Length 888;
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
138218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: ATM1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
C;Keywords: ATP; phosphotransferase
F;24-293/Domain: protein kinase homology <KIN>
F;32-40/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Identification of 21 novel human protein kinases, A;Reference number: I38211; MUID:94100173; PMID:8274451 A;Accession: I38218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-serine/threonine kinase - human (fragment)
C;Species: Homo saptens (man)
C;Date: 06-Sep-1956 #sequence_revision 06-Sep-1956 #text_change 24-Sep-1959
C;Date: 05-Sep-1956 #sequence_revision 06-Sep-1956 #text_change 24-Sep-1959
C;Accession: 138218; S37420
                                                                                                                                                                                   C;Accession: T05675
R;Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뫄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-111 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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A; Residues: 1-356 <TRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: An unusual A; Reference number: S61766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell Growth Differ.
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                                                     A; Molecule type: DNA
A; Residues: 1-545 <BEV>
A; Cross-references: EMBL: AL035540
                                                                                                                                                                                                                                                                                      C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Sate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S61766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                          A; Experimental source: cultivar Columbia; BAC clone F20M13
                                                                                                                                              A; Reference number: Z15420
A; Accession: T05675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X92728; NID:g1054632; PIDN:CAA63387.1; PID:g1054633
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F20M13.30 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 HRDLKPENLIL--SADH-----KTVKLADFGLARE-ESLTEMMTAETGTYRWMAPE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 HRDLKSPNVL----VTHTD----AVKISDFGTSKELSDKSTKMSFAGTVAWMAPE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRTTKMSTA--GTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREW-HRTTKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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er. 4, 821-830, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 121; DB 2;
Pred. No. 6.3e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 121.5; DB 2; Pred. No. 1.8e-05;
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Indels 10;

Gaps

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A; Residues: 1-886 <BEV>
A; Cross-references: EMBL: AL163812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAP3K delta-1 protein kinase - Arabidopsis thaliana N;Alternate names: protein F14F18.20 C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-406 <JOU>
A;Cross-references: EMBL:Y14199; NID:g2253009; PIDN:CAA74591.1; PID:g2253010
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Characterisation of novel plant genes encoding MEKK/STE11 and RAF-related prote A; Reference number: Z24447; MUID:99196996; PMID:10095117 A; Accession: T52626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable mitogen-activated protein kinase MAP3K delta-1 [imported] - Arabidopsis thalian (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 08-Dec-2000 C;Accession: T52626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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A;Map position: 70/2; 108/3; 164/2; 204/2; 222/3; 259/3; 276/3; 328/2; 353/1; 411/3; 443/3; A;Note: F20M13.30
hypothetical protein F25P22.8 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 5
A; Introns: 148/3; 180/3; 327/3; 362/2; 568/3; 658/1; 671/3; 694/3; 728/2; 754/3; 810/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the Protein So
A; Reference number: Z24490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: cultivar Columbia; BAC clone F14F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T48544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Jouannic,
                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                     770 HRDLKSPN-LLVDK------NWVVKVCDFGLSRMKHHTYLSSKSTAGTPEWMAPE 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 HRDLKAANLIMDE-----NEVVKVADFGVARVKAQTGVMTAETGTYRWMAPE 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 HRDLKSPN-LLVDK-----NWVVKVCDFGLSRMKHHTYLSSKSTAGTPEWMAPE 303
                                                                                                                                                                                                                                                                     Local Similarity es 27; Conserv
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                                                                                                                                                                                                           1 HRDIKAGNILLLEKIEHDDICNKTLKITDEGLAREWHRT--TKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRT--TKMSTAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRTTKMST-AGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o, S.; Hamal, A.; Leprince, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y. 171-81, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                        37.9%;
48.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Database, April 2000
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Pred. No. 0.00042;
9; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 111; DB 2; Length 406; Pred. No. 0.00071; B; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                           Score 111; DB 2;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                       DB 2; Length 886;
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                                                                                                                                                                                                                                                              11; Indels 10;
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                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-58, 'I', 60-1478 <L
A; Cross-references: EMBL: X60227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain S288C R; Miosga, T.; Boles, E.; Schaaff-Ge: Yeast 10, 1481-1488, 1994
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                                                                                                                                                                                                                                                                                                                                                    A;Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypas A;Reference number: $22285; MUID:92107166; PMID:1729597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevi A; Reference number: S50295; MUID:95176706; PMID:7871887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1478 <COS>
A; Cross-references: EMBL: M84389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
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A; Residues: 1-1030 <STO>
                                                                                                                                                                                                        A; Experimental source: strain EG123
                                                                                                                                                                                                                                                                                                                              A; Accession: S22285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-1478 <MIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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27; Conserv
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C; Accession: F96763

C; Accession: F96763

C; Accession: F96763

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005173; NID:g6692730; PIDN:AAF24836.1; GSPDB:GN00141
869 HRDLKSPN-LLVDK-----NWVVKVCDFGLSRMKHSTYLSSKSTAGTAEWMAPE 916
                                                      1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAREWHRT~-TKMSTAGTYAWWAPE 54
                                                                                                                                                                                                                37.9%;
                                                                                                                                                                                   Score 111; DB 2;
Pred. No. 0.0018;
8; Mismatches 1
                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                   Indels 10;
                                                                                                                                                                                   Gaps
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protein kinase BCK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)

R/Alternate names: protein J0906; protein kinase SLK1; protein kinase SSP31; protein

C;Species: Saccharomyces cerevisiae

C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 24-Sep-1999

C;Accession: S2011; S50298; S22285; S19061; J01432; S56872; S30794; J01118

R;Costigan, C.; Gebrung, S.; Snyder, M.

A;Title: A synthetic lethal screen identifies SLK1, a novel protein kinase homolog im

A;Reference number: S20117; MUID:92186847; PMID:1545797

A;Accession: S20117 Schaaff-Gerstenschlaeger, I.; Schmitt, S.; Zimmermann, F.K.

A;Cross-references: EMBL:X77923; NID:g640004; PIDN:CAA54896.1; PID:g640009 R;Lee, K.S.; Levin, D.E. Mol. Cell. Biol. 12, 172-182, 1992

60-1478 <LEE>

R; Lee, K.S.; Levin, D.E. submitted to the EMBL Data Library, June 1991

A;Description: An extragenic suppressor of mutations in the S. cerevisiae protein kin A;Reference number: 519061
A;Accession: S19061

A; Molecule type: DNA A; Residues: 1-58,'I',60-263,'P',265-278,'I',280-702,'S',707-708,'KP',714,'VITMTE',715

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R;Miosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, submitted to the Protein Sequence Database, September 1995 A;Reference number: $56855 A;Accession: $56872 A;Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March 1992
A; Reference number: S27437
A; Reference number: S27437
A; Reference number: S27437
A; Recession: S30794
A; Molecule type: DNA
A; Residues: 602-959, 'R', 961, 'R', 963-1085,'V', 1087, 'SLLIAHT', 1092-1094, 'RMD', 1101, 'TV', 11
A; Cross-references: EMBL:M88604; NID:g172073; PIDN:AAA21179.1; PID:g172074
C; Genetics:
A; Gene: SGD:BCK1; SLK1; SSP31
A; Gross-references: SGD:S0003631; MIPS:YJL095W
A; Map position: 10L
C; Function:
A; Description: phosphotransferase; protein kinase; involved in cell proliferation
C; Supperfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C; Supperfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
C; Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;1173-1440/Domain: protein kinase homology <KIN>
F;1181-1189/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: A new protein kinase, SSP31, modulating the SMP3 gene-product involved in A;Reference number: JQ1432; MUID:92104496; PMID:1840547 A;Accession: JQ1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X60227; NID:g3414; PIDN:CAA42788.1; PID:g3415
A;Experimental source: strain EG123
R;Irie, K.; Araki, H.; Oshima, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable protein kinase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002 C;Accession: G84635 C;Accession: G84635 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
G84635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1478 <MIW>
A;Cross-references: EMBL:249370; NID:g1008269; PIDN:CAA89389.1; PID:g1008270; MIPS:YJL09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A: Residues: 1-1478 < MIW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Cusick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
밁
                                             Qy
                                                                                                                                                                                                              A;Gene: At2g24360
A;Map position: 2
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE002093; NID:g4337195; PIDN:AAD18109.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-407 <STO>
                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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                                                                                                                               Query Match
Best Local S
                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.; Araki, H.;
8, 139-144, 1991
250 HRDLKSDNLLI------SADKSIKIADFGVARIEVQTEGMTPETGTYRWMAPE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HRDIKAGNILLLEKIEHDDICNKTLKITDFGLAR---EWHRTTKMSTAGTYAWMAPE 54
                                                                                                                                    Local Similarity
                            1 HRDIKAGNILLLEKIEHDDICNKTLKITDEGLAREWHRTTKMS-TAGTYAWMAPE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                           Conservative
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                                                                                                     36.7%; Score 107.5; DB 2;
43.6%; Pred. No. 0.0016;
tive 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108.5; DB 2; Pred. No. 0.0044; 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                    Length 407;
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                                                                                                              Indels
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                                                                                                              9;
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Search completed: December 13, 2002, 23:32:06 Job time : 48 secs

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